

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Regents of the University of Minnesota
- (ii) TITLE OF THE INVENTION: ANALYSIS OF ALPHA INTEGRINS FOR THE DIAGNOSIS OF DIABETIC NEPHROPATHY
- (iii) NUMBER OF SEQUENCES: 16
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Merchant & Gould
 - (B) STREET: 3100 Norwest Center
90 South 7th Street
 - (C) CITY: Minneapolis
 - (D) STATE: MN
 - (E) COUNTRY: US
 - (F) ZIP: 55402
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ Version 1.5
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: Unknown
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Kettelberger, Denise
 - (B) REGISTRATION NUMBER: 33,924
 - (C) REFERENCE/DOCKET NUMBER: 600.314USWO
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 612-332-5300
 - (B) TELEFAX: 612-332-9081
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3987 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 420...3959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGTATGGAGA	GAAGGTCGTT	TAAAAAGGCA	GATGTCCTT	TAAGGTTTGC	TTTGCTGCTG	60										
CCCGTGGACT	TTAGCCTAAA	CAGGGTCCCG	CGAAGTTGGC	TTTATTTGTC	CATGTCCTCGG	120										
ACACAGCCTG	GGTAGCTGCC	AGTGAGATT	CAGGGACGGA	GCGCGCAAAG	GGGGGGGAAA	180										
TGTGGCAATC	CATCTGGGAT	GTGAGACGCG	TGGAGAGGGC	TTAGCAGCAT	TTGACCAAAA	240										
CACAGGAAAT	CACTCCTCCA	CAGCTCCTGG	GCGCAGCAGC	GGCTGGGGCC	ACTGCCGGAC	300										
ACCCCTCGGAG	ACCACACGAG	TGACCCAGAG	CGCAAGTCGC	CAGCGTCCCG	GTTCTGCCTG	360										
TTCCCTGCCAG	CTCCTGCCCA	CGAACCGGCA	CGTAGCTGGT	TCCAGCAGCC	GCTCCAGCA	419										
ATG GTC CCC AGG CGT CCT GCC AGC CTA GAG GTC ACT GTA GCC TGC ATA						467										
Met	Val	Pro	Arg	Arg	Pro	Ala	Ser	Leu	Glu	Val	Thr	Val	Ala	Cys	Ile	
-28	-25				-20								-15			
TGG CTT CTC ACG GTC ATC CTA GGC TTC TGC GTC TCC TTC AAT GTT GAT						515										
Trp	Leu	Leu	Thr	Val	Ile	Leu	Gly	Phe	Cys	Val	Ser	Phe	Asn	Val	Asp	
-10				-5									1			
GTG AAA AAC TCA ATG AGT TTC AGT GGC CCA GTA GAG GAC ATG TTT GGA						563										
Val	Lys	Asn	Ser	Met	Ser	Phe	Ser	Gly	Pro	Val	Glu	Asp	Met	Phe	Gly	
5				10						15			20			
TAC ACT GTT CAA CAA TAT GAA AAC GAA GAA GGC AAA TGG GTT CTT ATT						611										
Tyr	Thr	Val	Gln	Gln	Tyr	Glu	Asn	Glu	Glu	Gly	Lys	Trp	Val	Leu	Ile	
			25					30					35			
GGT TCT CCT TTA GTT GGC CAA CCC AAA GCA AGA ACT GGA GAT GTC TAT						659										
Gly	Ser	Pro	Leu	Val	Gly	Gln	Pro	Lys	Ala	Arg	Thr	Gly	Asp	Val	Tyr	
			40					45					50			
AAG TGT CCG GTT GGG AGA GAG AGA GCA ATG CCT TGC GTG AAG TTG GAC						707										
Lys	Cys	Pro	Val	Gly	Arg	Glu	Arg	Ala	Met	Pro	Cys	Val	Lys	Leu	Asp	
			55					60					65			

TTG CCA GTT AAC ACA TCG ATC CCC AAT GTC ACA GAA ATA AAG GAA AAC	755
Glu Pro Val Asn Thr Ser Ile Pro Asn Val Thr Glu Ile Lys Glu Asn	
70 75 80	
ATG ACA TTT GGA TCA ACT TTA GTC ACC AAC CCG AAT GGA GGA TTT CTG	803
Met Thr Phe Gly Ser Thr Leu Val Thr Asn Pro Asn Gly Gly Phe Leu	
85 90 95 100	
GCA TGT GGG CCC TTG TAT GCC TAT AGA TGT GGA CAT TTG CAT TAT ACA	851
Ala Cys Gly Pro Leu Tyr Ala Tyr Arg Cys Gly His Leu His Tyr Thr	
105 110 115	
ACT GGA ATA TGT TCT GAT GTC AGT CCT ACA TTT CAA GTT GTG AAC TCC	899
Thr Gly Ile Cys Ser Asp Val Ser Pro Thr Phe Gln Val Val Asn Ser	
120 125 130	
TTT GCC CCT GTA CAA GAA TGC AGC ACC CAG CTG GAC ATA GTC ATC GTC	947
Phe Ala Pro Val Gln Glu Cys Ser Thr Gln Leu Asp Ile Val Ile Val	
135 140 145	
CTG GAT GGC TCC AAC AGC ATC TAC CCC TGG GAA AGT GTC ATC GCC TTT	995
Leu Asp Gly Ser Asn Ser Ile Tyr Pro Trp Glu Ser Val Ile Ala Phe	
150 155 160	
TTA AAC GAC CTT CTT AAG AGG ATG GAT ATT GGC CCT AAG CAG ACA CAG	1043
Leu Asn Asp Leu Leu Lys Arg Met Asp Ile Gly Pro Lys Gln Thr Gln	
165 170 175 180	
GTC GGG ATT GTA CAG TAT GGA GAG AAT GTA ACC CAT GAG TTC AAC CTC	1091
Val Gly Ile Val Gln Tyr Gly Glu Asn Val Thr His Glu Phe Asn Leu	
185 190 195	
AAT AAG TAT TCA TCC ACA GAA GAG GTC CTT GTC GCA GCA AAC AAA ATA	1139
Asn Lys Tyr Ser Ser Thr Glu Glu Val Leu Val Ala Ala Asn Lys Ile	
200 205 210	
GGC CGA CAG GGA GGC CTC CAA ACG ATG ACA GCC CTT GGA ATA GAC ACA	1187
Gly Arg Gln Gly Leu Gln Thr Met Thr Ala Leu Gly Ile Asp Thr	
215 220 225	
GCC AGG AAA GAG GCA TTC ACT GAA GCT CGG GGT GCC AGG AGG GGA GTT	1235
Ala Arg Lys Glu Ala Phe Thr Glu Ala Arg Gly Ala Arg Arg Gly Val	
230 235 240	
AAA AAA GTC ATG GTT ATT GTG ACC GAC GGA GAA TCG CAT GAC AAC TAT	1283
Lys Lys Val Met Val Ile Val Thr Asp Gly Glu Ser His Asp Asn Tyr	
245 250 255 260	
CGC TGA AAC AGG TCA TCC AAG ACT GCG AGG ACG AAA ACA TTC AGC GAT	1331
Arg Leu Lys Gln Val Ile Gln Asp Cys Glu Asp Glu Asn Ile Gln Arg	
265 270 275	
TTT TCC ATA GCT ATC CTT GGC CAC TAT AAC AGG GGG AAC TTA AGC ACT	1379
Phe Ser Ile Ala Ile Leu Gly His Tyr Asn Arg Gly Asn Leu Ser Thr	
280 285 290	

GAA AAA TTT GTG GAG GAA ATA AAA TCG ATC GCA AGC GAG CCC ACG GAA Glu Lys Phe Val Glu Glu Ile Lys Ser Ile Ala Ser Glu Pro Thr Glu 295 300 305	1427
AAG CAC TTC TTC AAT GTC TCG GAT GAG TTG GCC CTG GTC ACT ATT GTT Lys His Phe Phe Asn Val Ser Asp Glu Leu Ala Leu Val Thr Ile Val 310 315 320	1475
AAA GCT CTG GGA GAA AGG ATA TTC GCT TTG GAA GCG ACA GCT GAC CAG Lys Ala Leu Gly Glu Arg Ile Phe Ala Leu Glu Ala Thr Ala Asp Gln 325 330 335 340	1523
TCA GCA GCT TCA TTT GAG ATG GAA ATG TCT CAG ACT GGC TTC AGT GCT Ser Ala Ala Ser Phe Glu Met Glu Met Ser Gln Thr Gly Phe Ser Ala 345 350 355	1571
CAC TAC TCC CAG GAC TGG GTC ATG CTT GGA GCG GTG GGA GCC TAT GAC His Tyr Ser Gln Asp Trp Val Met Leu Gly Ala Val Gly Ala Tyr Asp 360 365 370	1619
TGG AAC GGA ACT GTG GTC ATG CAG AAG GCT AAC CAG ATG GTC ATC CCT Trp Asn Gly Thr Val Val Met Gln Lys Ala Asn Gln Met Val Ile Pro 375 380 385	1667
CAT AAC ACC ACC TTT CAA ACT GAG CCC GCC AAG ATG AAC GAG CCT CTG His Asn Thr Thr Phe Gln Thr Glu Pro Ala Lys Met Asn Glu Pro Leu 390 395 400	1715
GCT TCT TAT TTA GGT TAC ACA GTG AAC TCG GCC ACC ATC CCT GGA GAT Ala Ser Tyr Leu Gly Tyr Thr Val Asn Ser Ala Thr Ile Pro Gly Asp 405 410 415 420	1763
GTG CTC TAC ATC GCT GGG CAG CCT CGG TAC AAT CAT ACG GGC CAG GTC Val Leu Tyr Ile Ala Gly Gln Pro Arg Tyr Asn His Thr Gly Gln Val 425 430 435	1811
GTC ATC TAC AAG ATG GAG GAT GGG AAC ATC AAC ATT CTG CAG ACA CTC Val Ile Tyr Lys Met Glu Asp Gly Asn Ile Asn Ile Leu Gln Thr Leu 440 445 450	1859
GGC GGA GAG CAG ATT GGT TCC TAC TTT GGT AGT GTC TTA ACA ACA ATT Gly Gly Glu Gln Ile Gly Ser Tyr Phe Gly Ser Val Leu Thr Thr Ile 455 460 465	1907
GAC ATC GAC AAA GAT TCT TAT ACT GAT CTG CTT CTC GTC GGG GCC CCC Asp Ile Asp Lys Asp Ser Tyr Thr Asp Leu Leu Leu Val Gly Ala Pro 470 475 480	1955
ATG TAC ATG GGG ACA GAG AAA GAG GAA CAG GGC AAG GTG TAC GTG TAC Met Tyr Met Gly Thr Glu Lys Glu Glu Gln Gly Lys Val Tyr Val Tyr 485 490 495 500	2003
GCT GTG AAT CAG ACA AGG TTT GAA TAT CAA ATG AGC CTG GAA CCA ATT Ala Val Asn Gln Thr Arg Phe Glu Tyr Gln Met Ser Leu Glu Pro Ile 505 510 515	2051

GGC AGA CCT GCT GCT CAT CCC TGA AGG ATA ATT CAT GCA CGA AAG AAA	520	525	530	2099
Arg Gln Thr Cys Cys Ser Ser Leu Lys Asp Asn Ser Cys Thr Lys Glu				
AAC AAG AAT GAG CCC TGC GGG GCC CGC TTC GGA ACA GCA ATT GCT GCT	535	540	545	2147
Asn Lys Asn Glu Pro Cys Gly Ala Arg Phe Gly Thr Ala Ile Ala Ala				
GTA AAA GAC CTC AAC GTG GAT GGA TTT AAT GAC GTC GTG ATT GGA GCT	550	555	560	2195
Val Lys Asp Leu Asn Val Asp Gly Phe Asn Asp Val Val Ile Gly Ala				
CCG CTG GAA GAT GAC CAC GCA GGA GCT GTG TAC ATT TAT CAT GGC AGT	565	570	575	2243
Pro Leu Glu Asp Asp His Ala Gly Ala Val Tyr Ile Tyr His Gly Ser				
GGC AAG ACC ATA AGG GAG GCG TAT GCA CAA CGC ATT CCA TCA GGT GGG	585	590	595	2291
Gly Lys Thr Ile Arg Glu Ala Tyr Ala Gln Arg Ile Pro Ser Gly Gly				
GAT GGC AAG ACC CTG AAA TTT TTC GGC CAG TCT ATC CAC GGA GAG ATG	600	605	610	2339
Asp Gly Lys Thr Leu Lys Phe Phe Gly Gln Ser Ile His Gly Glu Met				
GAT TTA AAT GGT GAC GGT CTG ACT GAC GTG ACC ATT GGA GGC CTT GGT	615	620	625	2387
Asp Leu Asn Gly Asp Gly Leu Thr Asp Val Thr Ile Gly Gly Leu Gly				
GGA GCA GCC CTC TTC TGG GCC AGA GAT GTG GCT GTA GTT AAA GTG ACC	630	635	640	2435
Gly Ala Ala Leu Phe Trp Ala Arg Asp Val Ala Val Val Lys Val Thr				
ATG AAT TTT GAA CCC AAT AAA GTG AAT ATT CAA AAG AAA AAC TGC CGT	645	650	655	2483
Met Asn Phe Glu Pro Asn Lys Val Asn Ile Gln Lys Lys Asn Cys Arg				
GTG GAG GGC AAA GAA ACA GTG TGC ATA AAT GCT ACA ATG TGT TTT CAT	665	670	675	2531
Val Glu Gly Lys Glu Thr Val Cys Ile Asn Ala Thr Met Cys Phe His				
GTG AAA TTA AAG TCT AAA GAG GAC TCA ATT TAC GAG GCT GAT CTG CAG	680	685	690	2579
Val Lys Leu Lys Ser Lys Glu Asp Ser Ile Tyr Glu Ala Asp Leu Gln				
TAC CGT GTC ACC CTT GAT TCA CTG AGG CAG ATA TCA CGG AGC TTT TTT	695	700	705	2627
Tyr Arg Val Thr Leu Asp Ser Leu Arg Gln Ile Ser Arg Ser Phe Phe				
TCT GGA ACT CAG GAA AGG AAG ATT CAA AGA AAT ATC ACC GTT CGA GAA	710	715	720	2675
Ser Gly Thr Gln Glu Arg Lys Ile Gln Arg Asn Ile Thr Val Arg Glu				
TCA GAA TGC ATC AGG CAC TCC TTC TAC ATG TTG GAC AAA CAT GAC TTT	725	730	735	2723
Ser Glu Cys Ile Arg His Ser Phe Tyr Met Leu Asp Lys His Asp Phe				

CAG GAC TCT GTG AGA GTG ACT CTG GAT TTT AAT CTC ACT GAT CCA GAA Gln Asp Ser Val Arg Val Thr Leu Asp Phe Asn Leu Thr Asp Pro Glu 745 750 755	2771
AAT GGT CCT GTA CTT GAT GAC GCT CTG CCA AAC TCA GTC CAC GAA CAC Asn Gly Pro Val Leu Asp Asp Ala Leu Pro Asn Ser Val His Glu His 760 765 770	2819
ATT CCC TTT GCC AAA GAC TGT GGA AAC AAG GAA AGA TGC ATT TCA GAC Ile Pro Phe Ala Lys Asp Cys Gly Asn Lys Glu Arg Cys Ile Ser Asp 775 780 785	2867
CTC ACT CTG AAT GTG TCC ACC ACA GAA AAG AGC CTG CTG ATC GTC AAG Leu Thr Leu Asn Val Ser Thr Thr Glu Lys Ser Leu Leu Ile Val Lys 790 795 800	2915
TCC CAG CAT GAC AAG TTC AAC GTT AGC CTC ACC GTC AAA AAC AAA GGA Ser Gln His Asp Lys Phe Asn Val Ser Leu Thr Val Lys Asn Lys Gly 805 810 815 820	2963
GAC AGT GCG TAC AAC ACC AGG ACA GTG GTG CAG CAT TCA CCA AAT CTG Asp Ser Ala Tyr Asn Thr Arg Thr Val Val Gln His Ser Pro Asn Leu 825 830 835	3011
ATT TTT TCG GGA ATT GAG GAG ATC CAA AAA GAT AGC TGT GAA TCT AAT Ile Phe Ser Gly Ile Glu Glu Ile Gln Lys Asp Ser Cys Glu Ser Asn 840 845 850	3059
CAA AAT ATC ACT TGC AGA GTT GGA TAT CCT TTC CTA AGA GCA GGA GAA Gln Asn Ile Thr Cys Arg Val Gly Tyr Pro Phe Leu Arg Ala Gly Glu 855 860 865	3107
ACG GTT ACC TTC AAA ATA ATA TTC CAG TTT AAC ACA TCC CAT CTC TCG Thr Val Thr Phe Lys Ile Ile Phe Gln Phe Asn Thr Ser His Leu Ser 870 875 880	3155
GAA AAT GCA ATC ATT CAC TTA AGT GCA ACA AGT GAC AGT GAG GAG CCC Glu Asn Ala Ile Ile His Leu Ser Ala Thr Ser Asp Ser Glu Glu Pro 885 890 895 900	3203
CTG GAA TCT CTT AAT GAT AAT GAA GTA AAT ATT TCC ATC CCA GTA AAA Leu Glu Ser Leu Asn Asp Asn Glu Val Asn Ile Ser Ile Pro Val Lys 905 910 915	3251
TAT GAA GTT GGA CTG CAG TTT TAC AGT TCT GCG AGT GAA CAT CAC ATT Tyr Glu Val Gly Leu Gln Phe Tyr Ser Ser Ala Ser Glu His His Ile 920 925 930	3299
TCA GTC GCT GCC AAT GAG ACG ATC CCT GAG TTT ATT AAC TCC ACT GAG Ser Val Ala Ala Asn Glu Thr Ile Pro Glu Phe Ile Asn Ser Thr Glu 935 940 945	3347
GAC ATT GGG AAT GAA ATT AAT GTC TTC TAT ACG ATT AGA AAG AGG GGG Asp Ile Gly Asn Glu Ile Asn Val Phe Tyr Thr Ile Arg Lys Arg Gly 950 955 960	3395

CAT TTC CCA ATG CCA GAA CTT CAG CTG TCA ATT TCA TTC CCC AAT TTG		3443
His Phe Pro Met Pro Glu Leu Gln Leu Ser Ile Ser Phe Pro Asn Leu		
965 970 975 980		
ACG GCA GAT GGT TAT CCT GTA CTG TAC CCA ATT GGA TGG TCA TCT TCA		3491
Thr Ala Asp Gly Tyr Pro Val Leu Tyr Pro Ile Gly Trp Ser Ser Ser		
985 990 995		
GAT AAT GTG AAC TGT AGA CCC CGG AGC CTT GAG GAC CCC TTT GCC ATC		3539
Asp Asn Val Asn Cys Arg Pro Arg Ser Leu Glu Asp Pro Phe Gly Ile		
1000 1005 1010		
AAC TCT GGG AAG AAA ATG ACA ATA TCG AAG TCT GAG GTT CTC AAA AGA		3587
Asn Ser Gly Lys Lys Met Thr Ile Ser Lys Ser Glu Val Leu Lys Arg		
1015 1020 1025		
GGC ACA ATC CAG GAC TGC AGT AGT ACG TGT GGA GTT GCC ACC ATC ACG		3635
Gly Thr Ile Gln Asp Cys Ser Ser Thr Cys Gly Val Ala Thr Ile Thr		
1030 1035 1040		
TGT AGC CTC CTT CCT TCC GAC CTG AGT CAA GTG AAT GTC TCG CTC CTC		3683
Cys Ser Leu Leu Pro Ser Asp Leu Ser Gln Val Asn Val Ser Leu Leu		
1045 1050 1055 1060		
CTG TGG AAA CCG ACT TTC ATA AGA GCA CAT TTT TCC AGC TTA AAC CTT		3731
Leu Trp Lys Pro Thr Phe Ile Arg Ala His Phe Ser Ser Leu Asn Leu		
1065 1070 1075		
ACT CTA AGA GGA GAA CTT AAG AGT GAA AAT TCA TCG CTG ACT TTA AGT		3779
Thr Leu Arg Gly Glu Leu Lys Ser Glu Asn Ser Ser Leu Thr Leu Ser		
1080 1085 1090		
AGC AGC AAC CGG AAG CGA GAG CTG GCT ATT CAG ATA TCC AAA GAC GGG		3827
Ser Ser Asn Arg Lys Arg Glu Leu Ala Ile Gln Ile Ser Lys Asp Gly		
1095 1100 1105		
CTC CCA GGC AGA GTG CCG CTG TGG GTT ATC CTC CTG AGC GCC TTC GCG		3875
Leu Pro Gly Arg Val Pro Leu Trp Val Ile Leu Leu Ser Ala Phe Ala		
1110 1115 1120		
GGG CTA CTG CTG CTA ATG CTC CTT ATA TTG GCT CTG TGG AAG ATT GGA		3923
Gly Leu Leu Leu Leu Met Leu Leu Ile Leu Ala Leu Trp Lys Ile Gly		
1125 1130 1135 1140		
TTC TTC AAA AGG CCA CTG AAG AAG AAA ATG GAG AAA TGAAAGGTTT		3969
Phe Phe Lys Arg Pro Leu Lys Lys Lys Met Glu Lys		
1145 1150		
CATAGAAAAA AAAAAAAA		3987

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Val Pro Arg Arg Pro Ala Ser Leu Glu Val Thr Val Ala Cys Ile
-28 -25 -20 -15

Trp Leu Leu Thr Val Ile Leu Gly Phe Cys Val Ser Phe Asn Val Asp
-10 -5 1

Val Lys Asn Ser Met Ser Phe Ser Gly Pro Val Glu Asp Met Phe Gly
5 10 15 20

Tyr Thr Val Gln Gln Tyr Glu Asn Glu Glu Gly Lys Trp Val Leu Ile
25 30 35

Gly Ser Pro Leu Val Gly Gln Pro Lys Ala Arg Thr Gly Asp Val Tyr
40 45 50

Lys Cys Pro Val Gly Arg Glu Arg Ala Met Pro Cys Val Lys Leu Asp
55 60 65

Glu Pro Val Asn Thr Ser Ile Pro Asn Val Thr Glu Ile Lys Glu Asn
70 75 80

Met Thr Phe Gly Ser Thr Leu Val Thr Asn Pro Asn Gly Gly Phe Leu
85 90 95 100

Ala Cys Gly Pro Leu Tyr Ala Tyr Arg Cys Gly His Leu His Tyr Thr
105 110 115

Thr Gly Ile Cys Ser Asp Val Ser Pro Thr Phe Gln Val Val Asn Ser
120 125 130

Phe Ala Pro Val Gln Glu Cys Ser Thr Gln Leu Asp Ile Val Ile Val
135 140 145

Leu Asp Gly Ser Asn Ser Ile Tyr Pro Trp Glu Ser Val Ile Ala Phe
150 155 160

Leu Asn Asp Leu Leu Lys Arg Met Asp Ile Gly Pro Lys Gln Thr Gln
165 170 175 180

Val Gly Ile Val Gln Tyr Gly Glu Asn Val Thr His Glu Phe Asn Leu
185 190 195

Asn Lys Tyr Ser Ser Thr Glu Glu Val Leu Val Ala Ala Asn Lys Ile
 200 205 210

Gly Arg Gln Gly Gly Leu Gln Thr Met Thr Ala Leu Gly Ile Asp Thr
 215 220 225

Ala Arg Lys Glu Ala Phe Thr Glu Ala Arg Gly Ala Arg Arg Gly Val
 230 235 240

Lys Lys Val Met Val Ile Val Thr Asp Gly Glu Ser His Asp Asn Tyr
 245 250 255 260

Arg Leu Lys Gln Val Ile Gln Asp Cys Glu Asp Glu Asn Ile Gln Arg
 265 270 275

Phe Ser Ile Ala Ile Leu Gly His Tyr Asn Arg Gly Asn Leu Ser Thr
 280 285 290

Glu Lys Phe Val Glu Glu Ile Lys Ser Ile Ala Ser Glu Pro Thr Glu
 295 300 305

Lys His Phe Phe Asn Val Ser Asp Glu Leu Ala Leu Val Thr Ile Val
 310 315 320

Lys Ala Leu Gly Glu Arg Ile Phe Ala Leu Glu Ala Thr Ala Asp Gln
 325 330 335 340

Ser Ala Ala Ser Phe Glu Met Glu Met Ser Gln Thr Gly Phe Ser Ala
 345 350 355

His Tyr Ser Gln Asp Trp Val Met Leu Gly Ala Val Gly Ala Tyr Asp
 360 365 370

Trp Asn Gly Thr Val Val Met Gln Lys Ala Asn Gln Met Val Ile Pro
 375 380 385

His Asn Thr Thr Phe Gln Thr Glu Pro Ala Lys Met Asn Glu Pro Leu
 390 395 400

Ala Ser Tyr Leu Gly Tyr Thr Val Asn Ser Ala Thr Ile Pro Gly Asp
 405 410 415 420

Val Leu Tyr Ile Ala Gly Gln Pro Arg Tyr Asn His Thr Gly Gln Val
 425 430 435

Val Ile Tyr Lys Met Glu Asp Gly Asn Ile Asn Ile Leu Gln Thr Leu
 440 445 450

Gly Gly Glu Gln Ile Gly Ser Tyr Phe Gly Ser Val Leu Thr Thr Ile
 455 460 465

Asp Ile Asp Lys Asp Ser Tyr Thr Asp Leu Leu Leu Val Gly Ala Pro
 470 475 480

Met Tyr Met Gly Thr Glu Lys Glu Glu Gln Gly Lys Val Tyr Val Tyr
 485 490 495 500

Ala Val Asn Gln Thr Arg Phe Glu Tyr Gln Met Ser Leu Glu Pro Ile
505 510 515

Arg Gln Thr Cys Cys Ser Ser Leu Lys Asp Asn Ser Cys Thr Lys Glu
520 525 530

Asn Lys Asn Glu Pro Cys Gly Ala Arg Phe Gly Thr Ala Ile Ala Ala
535 540 545

Val Lys Asp Leu Asn Val Asp Gly Phe Asn Asp Val Val Ile Gly Ala
550 555 560

Pro Leu Glu Asp Asp His Ala Gly Ala Val Tyr Ile Tyr His Gly Ser
565 570 575 580

Gly Lys Thr Ile Arg Glu Ala Tyr Ala Gln Arg Ile Pro Ser Gly Gly
585 590 595

Asp Gly Lys Thr Leu Lys Phe Phe Gly Gln Ser Ile His Gly Glu Met
600 605 610

Asp Leu Asn Gly Asp Gly Leu Thr Asp Val Thr Ile Gly Gly Leu Gly
615 620 625

Gly Ala Ala Leu Phe Trp Ala Arg Asp Val Ala Val Val Lys Val Thr
630 635 640

Met Asn Phe Glu Pro Asn Lys Val Asn Ile Gln Lys Lys Asn Cys Arg
645 650 655 660

Val Glu Gly Lys Glu Thr Val Cys Ile Asn Ala Thr Met Cys Phe His
665 670 675

Val Lys Leu Lys Ser Lys Glu Asp Ser Ile Tyr Glu Ala Asp Leu Gln
680 685 690

Tyr Arg Val Thr Leu Asp Ser Leu Arg Gln Ile Ser Arg Ser Phe Phe
695 700 705

Ser Gly Thr Gln Glu Arg Lys Ile Gln Arg Asn Ile Thr Val Arg Glu
710 715 720

Ser Glu Cys Ile Arg His Ser Phe Tyr Met Leu Asp Lys His Asp Phe
725 730 735 740

Gln Asp Ser Val Arg Val Thr Leu Asp Phe Asn Leu Thr Asp Pro Glu
745 750 755

Asn Gly Pro Val Leu Asp Asp Ala Leu Pro Asn Ser Val His Glu His
760 765 770

Ile Pro Phe Ala Lys Asp Cys Gly Asn Lys Glu Arg Cys Ile Ser Asp
775 780 785

Leu Thr Leu Asn Val Ser Thr Thr Glu Lys Ser Leu Leu Ile Val Lys
790 795 800

Ser Gln His Asp Lys Phe Asn Val Ser Leu Thr Val Lys Asn Lys Gly
 805 810 815 820

Asp Ser Ala Tyr Asn Thr Arg Thr Val Val Gln His Ser Pro Asn Leu
 825 830 835

Ile Phe Ser Gly Ile Glu Glu Ile Gln Lys Asp Ser Cys Glu Ser Asn
 840 845 850

Gln Asn Ile Thr Cys Arg Val Gly Tyr Pro Phe Leu Arg Ala Gly Glu
 855 860 865

Thr Val Thr Phe Lys Ile Ile Phe Gln Phe Asn Thr Ser His Leu Ser
 870 875 880

Glu Asn Ala Ile Ile His Leu Ser Ala Thr Ser Asp Ser Glu Glu Pro
 885 890 895 900

Leu Glu Ser Leu Asn Asp Asn Glu Val Asn Ile Ser Ile Pro Val Lys
 905 910 915

Tyr Glu Val Gly Leu Gln Phe Tyr Ser Ser Ala Ser Glu His His Ile
 920 925 930

Ser Val Ala Ala Asn Glu Thr Ile Pro Glu Phe Ile Asn Ser Thr Glu
 935 940 945

Asp Ile Gly Asn Glu Ile Asn Val Phe Tyr Thr Ile Arg Lys Arg Gly
 950 955 960

His Phe Pro Met Pro Glu Leu Gln Leu Ser Ile Ser Phe Pro Asn Leu
 965 970 975 980

Thr Ala Asp Gly Tyr Pro Val Leu Tyr Pro Ile Gly Trp Ser Ser Ser
 985 990 995

Asp Asn Val Asn Cys Arg Pro Arg Ser Leu Glu Asp Pro Phe Gly Ile
 1000 1005 1010

Asn Ser Gly Lys Lys Met Thr Ile Ser Lys Ser Glu Val Leu Lys Arg
 1015 1020 1025

Gly Thr Ile Gln Asp Cys Ser Ser Thr Cys Gly Val Ala Thr Ile Thr
 1030 1035 1040

Cys Ser Leu Leu Pro Ser Asp Leu Ser Gln Val Asn Val Ser Leu Leu
 1045 1050 1055 1060

Leu Trp Lys Pro Thr Phe Ile Arg Ala His Phe Ser Ser Leu Asn Leu
 1065 1070 1075

Thr Leu Arg Gly Glu Leu Lys Ser Glu Asn Ser Ser Leu Thr Leu Ser
 1080 1085 1090

Ser Ser Asn Arg Lys Arg Glu Leu Ala Ile Gln Ile Ser Lys Asp Gly
 1095 1100 1105

Leu Pro Gly Arg Val Pro Leu Trp Val Ile Leu Leu Ser Ala Phe Ala
 1110 1115 1120

Gly Leu Leu Leu Leu Met Leu Leu Ile Leu Ala Leu Trp Lys Ile Gly
 1125 1130 1135 1140

Phe Phe Lys Arg Pro Leu Lys Lys Lys Met Glu Lys
 1145 1150

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 49...3591

(D) OTHER INFORMATION:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 136

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCCCTGC AAACCCAGCG CAACTACGGT CCCCCGGTCA GACCCAGG ATG GGG CCA 57
 Met Gly Pro
 -29

GAA CGG ACA GGG GCC GCG CCG CTG CCG CTG CTG CTG GTG TTA GCG CTC 105
 Glu Arg Thr Gly Ala Ala Pro Leu Pro Leu Leu Val Leu Ala Leu
 -25 -20 -15

AGT CAA GGC ATT TTA AAT TGT TGT TTG GCC TAC AAT GTT GGT CTC CCA 153
 Ser Gln Gly Ile Leu Asn Cys Cys Leu Ala Tyr Asn Val Gly Leu Pro
 -10 -5 1 5

GAA GCA AAA ATA TTT TCC GGT CCT TCA AGT GAA CAG TTT GGG TAT GCA 201
 Glu Ala Lys Ile Phe Ser Gly Pro Ser Ser Glu Gln Phe Gly Tyr Ala
 10 15 20

GTG CAG CAG TTT ATA AAT CCA AAA GGC AAC TGG TTA CTG GTT GGT TCA 249
 Val Gln Gln Phe Ile Asn Pro Lys Gly Asn Trp Leu Leu Val Gly Ser
 25 30 35

CCC TGG AGT GGC TTT CCT GAG AAC CGA ATG GGA GAT GTG TAT AAA TGT	297
Pro Trp Ser Gly Phe Pro Glu Asn Arg Met Gly Asp Val Tyr Lys Cys	
40 45 50	
CCT GTT GAC CTA TCC ACT GCC ACA TGT GAA AAA CTA AAT TTG CAA ACT	345
Pro Val Asp Leu Ser Thr Ala Thr Cys Glu Lys Leu Asn Leu Gln Thr	
55 60 65 70	
TCA ACA AGC ATT CCA AAT GTT ACT GAG ATG AAA ACC AAC ATG AGC CTC	393
Ser Thr Ser Ile Pro Asn Val Thr Glu Met Lys Thr Asn Met Ser Leu	
75 80 85	
GGC TTG ATC CTC ACC AGG AAC ATG GGA ACT GGA GGT TTT CTC ACA TGT	441
Gly Leu Ile Leu Thr Arg Asn Met Gly Thr Gly Gly Phe Leu Thr Cys	
90 95 100	
GGT CCT CTG TGG GCA CAG CAA TGT GGG AAT CAG TAT TAC ACA ACG GGT	489
Gly Pro Leu Trp Ala Gln Gln Cys Gly Asn Gln Tyr Tyr Thr Thr Gly	
105 110 115	
GTG TGT TCT GAC ATC AGT CCT GAT TTT CAG CTC TCA GCC AGC TTC TCA	537
Val Cys Ser Asp Ile Ser Pro Asp Phe Gln Leu Ser Ala Ser Phe Ser	
120 125 130	
CCT GCA ACT CAG CCC TGC CCT CTC ATA GAT GTT GTG GTT GTG TGT	585
Pro Ala Thr Gln Pro Cys Pro Ser Leu Ile Asp Val Val Val Val Cys	
135 140 145 150	
GAT GAA TCA AAT AGT ATT TAT CCT TGG GAT GCA GTA AAG AAT TTT TTG	633
Asp Glu Ser Asn Ser Ile Tyr Pro Trp Asp Ala Val Lys Asn Phe Leu	
155 160 165	
GAA AAA TTT GTA CAA GGC CTT GAT ATA GGC CCC ACA AAG ACA CAG GTG	681
Glu Lys Phe Val Gln Gly Leu Asp Ile Gly Pro Thr Lys Thr Gln Val	
170 175 180	
GGG TTA ATT CAG TAT GCC AAT AAT CCA AGA GTT GTG TTT AAC TTG AAC	729
Gly Leu Ile Gln Tyr Ala Asn Asn Pro Arg Val Val Phe Asn Leu Asn	
185 190 195	
ACA TAT AAA ACC AAA GAA GAA ATG ATT GTA GCA ACA TCC CAG ACA TCC	777
Thr Tyr Lys Thr Lys Glu Glu Met Ile Val Ala Thr Ser Gln Thr Ser	
200 205 210	
CAA TAT GGT GGG GAC CTC ACA AAC ACA TTC GGA GCA ATT CAA TAT GCA	825
Gln Tyr Gly Gly Asp Leu Thr Asn Thr Phe Gly Ala Ile Gln Tyr Ala	
215 220 225 230	
AGA AAA TAT GCC TAT TCA GCA GCT TCT GGT GGG CGA CGA AGT GCT ACG	873
Arg Lys Tyr Ala Tyr Ser Ala Ala Ser Gly Gly Arg Arg Ser Ala Thr	
235 240 245	
AAA GTA ATG GTA GTT GTA ACT GAC GGT GAA TCA CAT GAT GGT TCA ATG	921
Lys Val Met Val Val Val Thr Asp Gly Glu Ser His Asp Gly Ser Met	
250 255 260	

TTG AAA GCT GTG ATT GAT CAA TGC AAC CAT GAC AAT ATA CTG AGG TTT Leu Lys Ala Val Ile Asp Gln Cys Asn His Asp Asn Ile Leu Arg Phe 265 270 275	969
GGC ATA GCA GTT CTT GGG TAC TTA AAC AGA AAC GCC CTT GAT ACT AAA Gly Ile Ala Val Leu Gly Tyr Leu Asn Arg Asn Ala Leu Asp Thr Lys 280 285 290	1017
AAT TTA ATA AAA GAA ATA AAA GCG ATC GCT AGT ATT CCA ACA GAA AGA Asn Leu Ile Lys Glu Ile Lys Ala Ile Ala Ser Ile Pro Thr Glu Arg 295 300 305 310	1065
TAC TTT TTC AAT GTG TCT GAT GAA GCA GCT CTA CTA GAA AAG GCT GGG Tyr Phe Phe Asn Val Ser Asp Glu Ala Ala Leu Leu Glu Lys Ala Gly 315 320 325	1113
ACA TTA GGA GAA CAA ATT TTC AGC ATT GAA GGT ACT GTT CAA GGA GGA Thr Leu Gly Glu Gln Ile Phe Ser Ile Glu Gly Thr Val Gln Gly Gly 330 335 340	1161
GAC AAC TTT CAG ATG GAA ATG TCA CAA GTG GGA TTC AGT GCA GAT TAC Asp Asn Phe Gln Met Glu Met Ser Gln Val Gly Phe Ser Ala Asp Tyr 345 350 355	1209
TCT TCT CAA AAT GAT ATT CTG ATG CTG GGT GCA GTG GGA GCT TTT GGC Ser Ser Gln Asn Asp Ile Leu Met Leu Gly Ala Val Gly Ala Phe Gly 360 365 370	1257
TGG AGT GGG ACC ATT GTC CAG AAG ACA TCT CAT GGC CAT TTG ATC TTT Trp Ser Gly Thr Ile Val Gln Lys Thr Ser His Gly His Leu Ile Phe 375 380 385 390	1305
CCT AAA CAA GCC TTT GAC CAA ATT CTG CAG GAC AGA AAT CAC AGT TCA Pro Lys Gln Ala Phe Asp Gln Ile Leu Gln Asp Arg Asn His Ser Ser 395 400 405	1353
TAT TTA GGT TAC TCT GTG GCT GCA ATT TCT ACT GGA GAA AGC ACT CAC Tyr Leu Gly Tyr Ser Val Ala Ala Ile Ser Thr Gly Glu Ser Thr His 410 415 420	1401
TTT GTT GCT GGT GCT CCT CGG GCA AAT TAT ACC GGC CAG ATA GTG CTA Phe Val Ala Gly Ala Pro Arg Ala Asn Tyr Thr Gly Gln Ile Val Leu 425 430 435	1449
TAT AGT GTG AAT GAG AAT GGC AAT ATC ACG GTT ATT CAG GCT CAC CGA Tyr Ser Val Asn Glu Asn Gly Asn Ile Thr Val Ile Gln Ala His Arg 440 445 450	1497
GGT GAC CAG ATT GGC TCC TAT TTT GGT AGT GTG CTG TGT TCA GTT GAT Gly Asp Gln Ile Gly Ser Tyr Phe Gly Ser Val Leu Cys Ser Val Asp 455 460 465 470	1545
GTG GAT AAA GAC ACC ATT ACA GAC GTG CTC TTG GTA GGT GCA CCA ATG Val Asp Lys Asp Thr Ile Thr Asp Val Leu Leu Val Gly Ala Pro Met 475 480 485	1593

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TAC ATG AGT GAC CTA AAG AAA GAG GAA GGA AGA GTC TAC CTG TTT ACT			1641
Tyr Met Ser Asp Leu Lys Lys Glu Glu Gly Arg Val Tyr Leu Phe Thr			
490	495	500	
ATC AAA AAG GGC ATT TTG GGT CAG CAC CAA TTT CTT GAA GGC CCC GAG			1689
Ile Lys Lys Gly Ile Leu Gly Gln His Gln Phe Leu Glu Gly Pro Glu			
505	510	515	
GGC ATT GAA AAC ACT CGA TTT GGT TCA GCA ATT GCA GCT CTT TCA GAC			1737
Gly Ile Glu Asn Thr Arg Phe Gly Ser Ala Ile Ala Ala Leu Ser Asp			
520	525	530	
ATC AAC ATG GAT GGC TTT AAT GAT GTG ATT GTT GGT TCA CCA CTA GAA			1785
Ile Asn Met Asp Gly Phe Asn Asp Val Ile Val Gly Ser Pro Leu Glu			
535	540	545	550
AAT CAG AAT TCT GGA GCT GTA TAC ATT TAC AAT GGT CAT CAG GGC ACT			1833
Asn Gln Asn Ser Gly Ala Val Tyr Ile Tyr Asn Gly His Gln Gly Thr			
555	560	565	
ATC CGC ACA AAG TAT TCC CAG AAA ATC TTG GGA TCC GAT GGA GCC TTT			1881
Ile Arg Thr Lys Tyr Ser Gln Lys Ile Leu Gly Ser Asp Gly Ala Phe			
570	576	580	
AGG AGC CAT CTC CAG TAC TTT GGG AGG TCC TTG GAT GGC TAT GGA GAT			1929
Arg Ser His Leu Gln Tyr Phe Gly Arg Ser Leu Asp Gly Tyr Gly Asp			
585	590	595	
TTA AAT GGG GAT TCC ATC ACC GAT GTG TCT ATT GGT GCC TTT GGA CAA			1977
Leu Asn Gly Asp Ser Ile Thr Asp Val Ser Ile Gly Ala Phe Gly Gln			
600	605	610	
GTG GTT CAA CTC TGG TCA CAA AGT ATT GCT GAT GTA GCT ATA GAA GCT			2025
Val Val Gln Leu Trp Ser Gln Ser Ile Ala Asp Val Ala Ile Glu Ala			
615	620	625	630
TCA TTC ACA CCA GAA AAA ATC ACT TTG GTC AAC AAG AAT GCT CAG ATA			2073
Ser Phe Thr Pro Glu Lys Ile Thr Leu Val Asn Lys Asn Ala Gln Ile			
635	640	645	
ATT CTC AAA CTC TGC TTC AGT GCA AAG TTC AGA CCT ACT AAG CAA AAC			2121
Ile Leu Lys Leu Cys Phe Ser Ala Lys Phe Arg Pro Thr Lys Gln Asn			
650	655	660	
AAT CAA GTG GCC ATT GTA TAT AAC ATC ACA CTT GAT GCA GAT GGA TTT			2169
Asn Gln Val Ala Ile Val Tyr Asn Ile Thr Leu Asp Ala Asp Gly Phe			
665	670	675	
TCA TCC AGA GTA ACC TCC AGG GGG TTA TTT AAA GAA AAC AAT GAA AGG			2217
Ser Ser Arg Val Thr Ser Arg Gly Leu Phe Lys Glu Asn Asn Glu Arg			
680	685	690	
TGC CTG CAG AAG AAT ATG GTA AAT CAA GCA CAG AGT TGC CCC GAG			2265
Cys Leu Gln Lys Asn Met Val Val Asn Gln Ala Gln Ser Cys Pro Glu			
695	700	715	720

CAC ATC ATT TAT ATA CAG GAG CCC TCT GAT GTT GTC AAC TCT TTG GAT His Ile Ile Tyr Ile Gln Glu Pro Ser Asp Val Val Asn Ser Leu Asp 725 730 735	2313
TTG CGT GTG GAC ATC AGT CTG GAA AAC CCT GGC ACT AGC CCT GCC CTT Leu Arg Val Asp Ile Ser Leu Glu Asn Pro Gly Thr Ser Pro Ala Leu 740 745 750	2361
GAA GCC TAT TCT GAG ACT GCC AAG GTC TTC AGT ATT CCT TTC CAC AAA Glu Ala Tyr Ser Glu Thr Ala Lys Val Phe Ser Ile Pro Phe His Lys 755 760 765	2409
GAC TGT GGT GAG GAT GGA CTT TGC ATT TCT GAT CTA GTC CTA GAT GTC Asp Cys Gly Glu Asp Gly Leu Cys Ile Ser Asp Leu Val Leu Asp Val 760 765 770	2457
CGA CAA ATA CCA GCT GCT CAA GAA CAA CCC TTT ATT GTC AGC AAC CAA Arg Gln Ile Pro Ala Ala Gln Glu Gln Pro Phe Ile Val Ser Asn Gln 775 780 785 790	2505
AAC AAA AGG TTA ACA TTT TCA GTA ACA CTG AAA AAT AAA AGG GAA AGT Asn Lys Arg Leu Thr Phe Ser Val Thr Leu Lys Asn Lys Arg Glu Ser 795 800 805	2553
GCA TAC AAC ACT GGA ATT GTT GAT TTT TCA GAA AAC TTG TTT TTT Ala Tyr Asn Thr Gly Ile Val Val Asp Phe Ser Glu Asn Leu Phe Phe 810 815 820	2601
GCA TCA TTC TCC CTA CCG GTT GAT GGG ACA GAA GTA ACA TGC CAG GTG Ala Ser Phe Ser Leu Pro Val Asp Gly Thr Glu Val Thr Cys Gln Val 825 830 835	2649
GCT GCA TCT CAG AAG TCT GTT GCC TGC GAT GTA GGC TAC CCT GCT TTA Ala Ala Ser Gln Lys Ser Val Ala Cys Asp Val Gly Tyr Pro Ala Leu 840 845 850	2697
AAG AGA GAA CAA CAG GTG ACT TTT ACT ATT AAC TTT GAC TTC AAT CTT Lys Arg Glu Gln Gln Val Thr Phe Thr Ile Asn Phe Asp Phe Asn Leu 855 860 865 870	2745
CAA AAC CTT CAG AAT CAG GCG TCT CTC AGT TTC CAA GCC TTA AGT GAA Gln Asn Leu Gln Asn Gln Ala Ser Leu Ser Phe Gln Ala Leu Ser Glu 875 880 885	2793
AGC CAA GAA GAA AAC AAG GCT GAT AAT TTG GTC AAC CTC AAA ATT CCT Ser Gln Glu Glu Asn Lys Ala Asp Asn Leu Val Asn Leu Lys Ile Pro 890 895 900	2841
CTC CTG TAT GAT GCT GAA ATT CAC TTA ACA AGA TCT ACC AAC ATA AAT Leu Leu Tyr Asp Ala Glu Ile His Leu Thr Arg Ser Thr Asn Ile Asn 905 910 915	2889
TTT TAT GAA ATC TCT TCG GAT GGG AAT GTT CCT TCA ATC GTG CAC AGT Phe Tyr Glu Ile Ser Ser Asp Gly Asn Val Pro Ser Ile Val His Ser 920 925 930	2937

TTT GAA GAT GTT GGT CCA AAA TTC ATC TTC TCC CTG AAG GTA ACA ACA Phe Glu Asp Val Gly Pro Lys Phe Ile Phe Ser Leu Lys Val Thr Thr 935 940 945 950	2985
GGA AGT GTT CCA GTA AGC ATG GCA ACT GTA ATC ATC CAC ATC CCT CAG Gly Ser Val Pro Val Ser Met Ala Thr Val Ile Ile His Ile Pro Gln 955 960 965	3033
TAT ACC AAA GAA AAG AAC CCA CTG ATG TAC CTA ACT GGG GTG CAA ACA Tyr Thr Lys Glu Lys Asn Pro Leu Met Tyr Leu Thr Gly Val Gln Thr 970 975 980	3081
GAC AAG GCT GGT GAC ATC AGT TGT AAT GCA GAT ATC AAT CCA CTG AAA Asp Lys Ala Gly Asp Ile Ser Cys Asn Ala Asp Ile Asn Pro Leu Lys 985 990 995	3129
ATA GGA CAA ACA TCT TCT TCT GTA TCT TTC AAA AGT GAA AAT TTC AGG Ile Gly Gln Thr Ser Ser Val Ser Phe Lys Ser Glu Asn Phe Arg 1000 1005 1010	3177
CAC ACC AAA GAA TTG AAC TGC AGA ACT GCT TCC TGT AGT AAT GTT ACC His Thr Lys Glu Leu Asn Cys Arg Thr Ala Ser Cys Ser Asn Val Thr 1015 1020 1025 1030	3225
TGC TGG TTG AAA GAC GTT CAC ATG AAA GGA GAA TAC TTT GTT AAT GTG Cys Trp Leu Lys Asp Val His Met Lys Gly Glu Tyr Phe Val Asn Val 1035 1040 1045	3273
ACT ACC AGA ATT TGG AAC GGG ACT TTC GCA TCA TCA ACG TTC CAG ACA Thr Thr Arg Ile Trp Asn Gly Thr Phe Ala Ser Ser Thr Phe Gln Thr 1050 1055 1060	3321
GTA CAG CTA ACG GCA GCT GCA GAA ATC AAC ACC TAT AAC CCT GAG ATA Val Gln Leu Thr Ala Ala Glu Ile Asn Thr Tyr Asn Pro Glu Ile 1065 1070 1075	3369
TAT GTG ATT GAA GAT AAC ACT GTT ACG ATT CCC CTG ATG ATA ATG AAA Tyr Val Ile Glu Asp Asn Thr Val Thr Ile Pro Leu Met Ile Met Lys 1080 1085 1090	3417
CCT GAT GAG AAA GCC GAA GTA CCA ACA GGA GTT ATA ATA GGA AGT ATA Pro Asp Glu Lys Ala Glu Val Pro Thr Gly Val Ile Ile Gly Ser Ile 1095 1100 1105 1110	3465
ATT GCT GGA ATC CTT TTG CTG TTA GCT CTG GTT GCA ATT TTA TGG AAG Ile Ala Gly Ile Leu Leu Leu Ala Leu Val Ala Ile Leu Trp Lys 1115 1120 1125	3513
CTC GGC TTC TTC AAA AGA AAA TAT GAA AAG ATG ACC AAA AAT CCA GAT Leu Gly Phe Phe Lys Arg Lys Tyr Glu Lys Met Thr Lys Asn Pro Asp 1130 1135 1140	3561
GAG ATT GAT GAG ACC ACA GAG CTC AGT AGC TGAACCAGCA GACCTACCTG CAGT Glu Ile Asp Glu Thr Thr Glu Leu Ser Ser 1145 1150	3615

GGGAACCGGC	AGCATCCCAG	CCAGGGTTT	CTGTTGCGT	GCATGGATT	CTTTTTAAAT	3675
CCCATATTT	TTTATCATG	TCGTAGGTAA	ACTAACCTGG	TATTTAAGA	GAAAACGTGCA	3735
GGTCAGTTG	GATGAAGAAA	TTGTGGGGGG	TGGGGGAGGT	GCGGGGGCA	GGTAGGGAAA	3795
TAATAGGGAA	AATACCTATT	TTATATGATG	GGGGAAAAAA	AGTAATCTT	AAACTGGCTG	3855
GCCCAGAGTT	TACATTCTAA	TTTGCATTGT	GTCAAGAACAA	TGAAATGCTT	CCAAGCATGA	3915
CAACTTTAA	AGAAAAATAT	GATACTCTCA	GATTTAAGG	GGGAAAACGT	TTCTCTTTAA	3975
AATATTTGTC	TTTAAACAGC	AACTACAGAA	GTGGAAGTGC	TTGATATGTA	AGTACTTCCA	4035
CTTGTGTATA	TTTAATGAA	TATTGATGTT	AACAAGAGGG	GGAAACAAAA	CACAGGTTT	4095
TTCAATTAT	GCTGCTCATC	CAAAGTTGCC	ACAGATGATA	CTTCCAAGTG	ATAATTTTAT	4155
TTATAAACTA	GGTAAAATT	GTTGTTGGTT	CCTTTTATAC	CACGGCTGCC	CCTTCCACAC	4215
CCCATCTTGC	TCTAATGATC	AAAACATGCT	TGAATAACTG	AGCTTAGAGT	ATACCTCCTA	4275
TATGTCCATT	TAAGTTAGGA	GAGGGGGCGA	TATAGAGACT	AAGGCACAAA	ATTTTGTTTA	4335
AAACTCAGAA	TATAACATTT	ATGTAAAATC	CCATCTGCTA	GAAGCCCATC	CTGTGCCAGA	4395
GGAAGGAAAA	GGAGGAAATT	TCCTTTCTCT	TTTAGGAGGC	ACAACAGTTC	TCTTCTAGGA	4455
TTTGTGGC	TGACTGGCAG	TAACCTAGTG	AATTTTGAA	AGATGAGTAA	TTTCTTTGGC	4515
AACCTTCCCT	CTCCCTTACT	GAACCACTCT	CCCACCTCCT	GGTGGTACCA	TTATTATAGA	4575
AGCCCTCTAC	AGCCTGACTT	TCTCTCCAGC	GGTCCAAAGT	TATCCCCCTC	TTTACCCCTC	4635
ATCCAAAGTT	CCCACCTCTT	CAGGACAGCT	GCTGTGCATT	AGATATTAGG	GGGGAAAGTC	4695
ATCTGTTAA	TTTACACACT	TGCATGAATT	ACTGTATATA	AACTCCTTAA	CTTCAGGGAG	4755
CTATTTTCA	TTAGTGCTAA	ACAAGTAAGA	AAAATAAGCT	AGAGTGAATT	TCTAAATGTT	4815
GGAATGTTAT	GGGATGTAAGA	CAATGTAAG	AAAAACACTC	TCAGGATTTC	ACCAGAAGTT	4875
ACAGATGAGG	CACTGGAAAC	CACCACAAA	TTAGCAGGTG	CACCTCTGT	GGCTGTCTTG	4935
TTTCTGAAGT	ACTTTTCTT	CCACAAGAGT	GAATTGACC	TAGGCAAGTT	TGTTCAAAAG	4995
GTAGATCCTG	AGATGATTG	GTCAGATTGG	GATAAGGCC	AGCAATCTGC	ATTTAACAA	5055
GCACCCCCAGT	CACTAGGATG	CAGATGGACC	ACACTTGAG	AAACACCACC	CATTCTACT	5115
TTTGCACCT	TATTTCTCT	GTTCCTGAGC	CCCCACATTC	TCTAGGAGAA	ACTTAGATTA	5175
AAATTCACAG	ACACTACATA	TCTAAAGCTT	TGACAAGTCC	TTGACCTCTA	TAAACTTCAG	5235
AGTCCTCATT	ATAAAATGGG	AAGACTGAGC	TGGAGTTCAG	CAGTGATGCT	TTTTAGTTT	5295
AAAAGTCTAT	GATCTGATCT	GGACTTCCTA	TAATACAAAT	ACACAATCCT	CCAAGAATT	5355
		GACTTGGAAA	AGGAATTC			5373

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE: internal
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gly Pro Glu Arg Thr Gly Ala Ala Pro Leu Pro Leu Leu Val
 -29 -25 -20 -15

Leu Ala Leu Ser Gln Gly Ile Leu Asn Cys Cys Leu Ala Tyr Asn Val
 -10 -5 1

Gly Leu Pro Glu Ala Lys Ile Phe Ser Gly Pro Ser Ser Glu Gln Phe
 5 10 15

Gly Tyr Ala Val Gln Gln Phe Ile Asn Pro Lys Gly Asn Trp Leu Leu
20 25 30 35

Val Gly Ser Pro Trp Ser Gly Phe Pro Glu Asn Arg Met Gly Asp Val
40 45 50

Tyr Lys Cys Pro Val Asp Leu Ser Thr Ala Thr Cys Glu Lys Leu Asn
55 60 65

Leu Gln Thr Ser Thr Ser Ile Pro Asn Val Thr Glu Met Lys Thr Asn
70 75 80

Met Ser Leu Gly Leu Ile Leu Thr Arg Asn Met Gly Thr Gly Gly Phe
85 90 95

Leu Thr Cys Gly Pro Leu Trp Ala Gln Gln Cys Gly Asn Gln Tyr Tyr
100 105 110 115

Thr Thr Gly Val Cys Ser Asp Ile Ser Pro Asp Phe Gln Leu Ser Ala
120 125 130

Ser Phe Ser Pro Ala Thr Gln Pro Cys Pro Ser Leu Ile Asp Val Val
135 140 145

Val Val Cys Asp Glu Ser Asn Ser Ile Tyr Pro Trp Asp Ala Val Lys
150 155 160

Asn Phe Leu Glu Lys Phe Val Gln Gly Leu Asp Ile Gly Pro Thr Lys
165 170 175

Thr Gln Val Gly Leu Ile Gln Tyr Ala Asn Asn Pro Arg Val Val Phe
180 185 190 195

Asn Leu Asn Thr Tyr Lys Thr Lys Glu Glu Met Ile Val Ala Thr Ser
200 205 210

Gln Thr Ser Gln Tyr Gly Asp Leu Thr Asn Thr Phe Gly Ala Ile
215 220 225

Gln Tyr Ala Arg Lys Tyr Ala Tyr Ser Ala Ala Ser Gly Gly Arg Arg
230 235 240

Ser Ala Thr Lys Val Met Val Val Val Thr Asp Gly Glu Ser His Asp
245 250 255

Gly Ser Met Leu Lys Ala Val Ile Asp Gln Cys Asn His Asp Asn Ile
260 265 270 275

Leu Arg Phe Gly Ile Ala Val Leu Gly Tyr Leu Asn Arg Asn Ala Leu
280 285 290

Asp Thr Lys Asn Leu Ile Lys Glu Ile Lys Ala Ile Ala Ser Ile Pro
295 300 305

Thr Glu Arg Tyr Phe Phe Asn Val Ser Asp Glu Ala Ala Leu Leu Glu
310 315 320

Lys Ala Gly Thr Leu Gly Glu Gln Ile Phe Ser Ile Glu Gly Thr Val
325 330 335

Gln Gly Gly Asp Asn Phe Gln Met Glu Met Ser Gln Val Gly Phe Ser
340 345 350 355

Ala Asp Tyr Ser Ser Gln Asn Asp Ile Leu Met Leu Gly Ala Val Gly
360 365 370

Ala Phe Gly Trp Ser Gly Thr Ile Val Gln Lys Thr Ser His Gly His
375 380 385

Leu Ile Phe Pro Lys Gln Ala Phe Asp Gln Ile Leu Gln Asp Arg Asn
390 395 400

His Ser Ser Tyr Leu Gly Tyr Ser Val Ala Ala Ile Ser Thr Gly Glu
405 410 415

Ser Thr His Phe Val Ala Gly Ala Pro Arg Ala Asn Tyr Thr Gly Gln
420 425 430 435

Ile Val Leu Tyr Ser Val Asn Glu Asn Gly Asn Ile Thr Val Ile Gln
440 445 450

Ala His Arg Gly Asp Gln Ile Gly Ser Tyr Phe Gly Ser Val Leu Cys
455 460 465

Ser Val Asp Val Asp Lys Asp Thr Ile Thr Asp Val Leu Leu Val Gly
470 475 480

Ala Pro Met Tyr Met Ser Asp Leu Lys Lys Glu Glu Gly Arg Val Tyr
485 490 495

Leu Phe Thr Ile Lys Lys Gly Ile Leu Gly Gln His Gln Phe Leu Glu
500 505 510 515

Gly Pro Glu Gly Ile Glu Asn Thr Arg Phe Gly Ser Ala Ile Ala Ala
520 525 530

Leu Ser Asp Ile Asn Met Asp Gly Phe Asn Asp Val Ile Val Gly Ser
535 540 545

Pro Leu Glu Asn Gln Asn Ser Gly Ala Val Tyr Ile Tyr Asn Gly His
550 555 560

Gln Gly Thr Ile Arg Thr Lys Tyr Ser Gln Lys Ile Leu Gly Ser Asp
565 570 575

Gly Ala Phe Arg Ser His Leu Gln Tyr Phe Gly Arg Ser Leu Asp Gly
580 585 590 595

Tyr Gly Asp Leu Asn Gly Asp Ser Ile Thr Asp Val Ser Ile Gly Ala
600 605 610

Phe Gly Gln Val Val Gln Leu Trp Ser Gln Ser Ile Ala Asp Val Ala
615 620 625

Ile Glu Ala Ser Phe Thr Pro Glu Lys Ile Thr Leu Val Asn Lys Asn
 630 635 640

Ala Gln Ile Ile Leu Lys Leu Cys Phe Ser Ala Lys Phe Arg Pro Thr
 645 650 655

Lys Gln Asn Asn Gln Val Ala Ile Val Tyr Asn Ile Thr Leu Asp Ala
 660 665 670 675

Asp Gly Phe Ser Ser Arg Val Thr Ser Arg Gly Leu Phe Lys Glu Asn
 680 685 690

Asn Glu Arg Cys Leu Gln Lys Asn Met Val Val Asn Gln Ala Gln Ser
 695 700 705

Cys Pro Glu His Ile Ile Tyr Ile Gln Glu Pro Ser Asp Val Val Asn
 710 715 720

Ser Leu Asp Leu Arg Val Asp Ile Ser Leu Glu Asn Pro Gly Thr Ser
 725 730 735

Pro Ala Leu Glu Ala Tyr Ser Glu Thr Ala Lys Val Phe Ser Ile Pro
 740 745 750 755

Phe His Lys Asp Cys Gly Glu Asp Gly Leu Cys Ile Ser Asp Leu Val
 760 765 770

Leu Asp Val Arg Gln Ile Pro Ala Ala Gln Glu Gln Pro Phe Ile Val
 775 780 785

Ser Asn Gln Asn Lys Arg Leu Thr Phe Ser Val Thr Leu Lys Asn Lys
 790 795 800

Arg Glu Ser Ala Tyr Asn Thr Gly Ile Val Val Asp Phe Ser Glu Asn
 805 810 815

Leu Phe Phe Ala Ser Phe Ser Leu Pro Val Asp Gly Thr Glu Val Thr
 820 825 830 835

Cys Gln Val Ala Ala Ser Gln Lys Ser Val Ala Cys Asp Val Gly Tyr
 840 845 850

Pro Ala Leu Lys Arg Glu Gln Gln Val Thr Phe Thr Ile Asn Phe Asp
 855 860 865

Phe Asn Leu Gln Asn Leu Gln Asn Gln Ala Ser Leu Ser Phe Gln Ala
 870 875 880

Leu Ser Glu Ser Gln Glu Glu Asn Lys Ala Asp Asn Leu Val Asn Leu
 885 890 895

Lys Ile Pro Leu Leu Tyr Asp Ala Glu Ile His Leu Thr Arg Ser Thr
 900 905 910 915

Asn Ile Asn Phe Tyr Glu Ile Ser Ser Asp Gly Asn Val Pro Ser Ile
 920 925 930

Val His Ser Phe Glu Asp Val Gly Pro Lys Phe Ile Phe Ser Leu Lys
935 940 945

Val Thr Thr Gly Ser Val Pro Val Ser Met Ala Thr Val Ile Ile His
950 955 960

Ile Pro Gln Tyr Thr Lys Glu Lys Asn Pro Leu Met Tyr Leu Thr Gly
965 970 975

Val Gln Thr Asp Lys Ala Gly Asp Ile Ser Cys Asn Ala Asp Ile Asn
980 985 990 995

Pro Leu Lys Ile Gly Gln Thr Ser Ser Val Ser Phe Lys Ser Glu
1000 1005 1010

Asn Phe Arg His Thr Lys Glu Leu Asn Cys Arg Thr Ala Ser Cys Ser
1015 1020 1025

Asn Val Thr Cys Trp Leu Lys Asp Val His Met Lys Gly Glu Tyr Phe
1030 1035 1040

Val Asn Val Thr Thr Arg Ile Trp Asn Gly Thr Phe Ala Ser Ser Thr
1045 1050 1055

Phe Gln Thr Val Gln Leu Thr Ala Ala Ala Glu Ile Asn Thr Tyr Asn
1060 1065 1070 1075

Pro Glu Ile Tyr Val Ile Glu Asp Asn Thr Val Thr Ile Pro Leu Met
1080 1085 1090

Ile Met Lys Pro Asp Glu Lys Ala Glu Val Pro Thr Gly Val Ile Ile
1095 1100 1105

Gly Ser Ile Ile Ala Gly Ile Leu Leu Leu Ala Leu Val Ala Ile
1110 1115 1120

Leu Trp Lys Leu Gly Phe Phe Lys Arg Lys Tyr Glu Lys Met Thr Lys
1125 1130 1135

Asn Pro Asp Glu Ile Asp Glu Thr Thr Glu Leu Ser Ser
1140 1145 1150

SEQUENCE NUMBER

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCAGAGTCAC TCTCACAGAG

20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CACAGCGTAC ACGTACACC

19

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CACTTATAGA CATCTCCAG

19

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CATCCATGTT GATGTCTG

18

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CATGTGATTG ACCGTCAG

18

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCATATTGAA TTGCTCCGAA TGTG

24

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCGTATGCA CAACGCA

17

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCGACAGCTG ACCAGTCAGC A

21

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CACTCCTCCA CAGCTCCT

18

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ACATGTACTC ACTGG

15

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTCACATGTG GTCCTCTG

18

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTCCTGTTGA CCTATCCACT GC

22